

Petition under 37 C.F.R. §1.181 Address to: Mail Stop Amendment Commissioner for Patents P.O. Box 1450 Alexandria, VA 22313-1450	Attorney Docket No.	STAN-277
	Confirmation No.	7388
	First Named Inventor	CHU, GILBERT
	Application Number	10/686,322
	Filing Date	October 14, 2003
	Group Art Unit	1637
	Examiner Name	Calamita, Heather
Title: "METHODS AND COMPOSITIONS FOR DETERMINING RISK OF TREATMENT TOXICITY"		

Commissioner for Patents
 P.O. Box 1450
 Alexandria, VA 22313-1450

Sir:

Applicants respectfully request the Commissioner to review the restriction requirement in the above-captioned patent application.

As originally filed, the present application contained Claims 1 – 46. In the Office Communication of May 16, 2006, Claims 1-46 were subject to a restriction requirement in which the claims were drawn to three groups; Group I (claims 1-33) being a method of predicting susceptibility to undesirable toxicity; Group II (claims 34-41) drawn to a kit; and Group III (claims 42-46) drawn to a method of determining a set of sequences whose expression is predictive of a phenotype.

Applicants elected the invention of Group I without traverse. No reconsideration is requested for the grouping of the claims.

In addition to Groups I, II and III, the Examiner required Applicants to elect a single nucleotide or amino acid sequence, stating that "nucleotide sequences encoding different proteins are structurally distinct compounds and are unrelated to one another. These sequences are thus deemed to normally constitute independent and distinct inventions within the meaning of 35 U.S.C. 121.

Applicants understand that it is common practice to restrict composition claims to a single nucleotide sequence. However, the present invention, as currently formulated, does not

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recite a composition claim, nor does it recite the use of single polynucleotides, such as one might find in distinct inventions.

In response to the sequence election requirement, Applicants note that the present claims are drawn to a method wherein the expression of at least 10 distinct sequences is obtained for analysis, as set forth in Claims 17, 22 and 23; or including expression information from 50 distinct sequences, as set forth in Claims 20, 47 and 48. Such a complex expression profile provides for a robust prediction that is not obtained with profiling of a single sequence.

Applicants respectfully submit that the sequences themselves are not being claimed, as all of the sequences recited in the present application are publicly available and known in the art. Rather, Applicants have provided a means of utilizing information from multiple sequences. As the claims require a minimum of 10 sequences or use of 50 sequences, an election cannot be made of a single sequence.

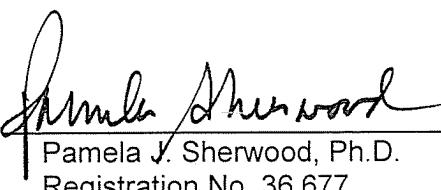
The difficulties of the Patent Office in searching is understood, however it is respectfully submitted that claims that recite obtaining expression data from at least 10 or 50 sequences are not usefully limited to a single polypeptide or polynucleotide sequence.

Applicants respectfully request reconsideration of the restriction.

The Commissioner is hereby authorized to charge any other fees under 37 C.F.R. §§ 1.16 and 1.17 which may be required by this paper, or to credit any overpayment, to Deposit Account No. 50-0815, order number STAN-277.

Respectfully submitted,
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Date: December 3, 2007

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